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Title of Manuscript:
Differential gene expression in Red Imported Fire Ant (*Solenopsis invicta*) (Hymenoptera: Formicidae) larval and pupal stages

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Prominent Issues:

- ☐ Potential to Attract Media Interest/Attention
☐ Represents a Significant Scientific Advancement
☐ Significantly Affect Existing or Future Policy
☐ Potential Trade Implications
☐ Other _____

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GRODOWITZ MICHAEL J	Entomology	4		6066-25-00

** Indicates approval of all Non-ARS authors of the Interpretive Summary, Technical Abstract and Affiliation to be released to the public.

Comments:

12/06/2018	Adding (Hymenoptera: Formicidae) to title; adding acceptance and publication date; generating citation. ayf
03/04/2018	Corrected the journal name from Journal of Insect Physiology to Journal of Insect Science. rwj
03/01/2018	Rejected by Journal of Insect Physiology and resubmitted to the Journal of Insect Science on 1/30/18. rwj
09/18/2017	Updated Date Submitted to Journal
09/12/2017	Establishing a 115 to be submitted to the Journal of Insect Physiology. ayf

Interpretive Summary:

Red imported fire ants are invasive biting and stinging pests, and are very difficult to control. A novel pest control method involving the interruption of gene activity could help subdue this pest. To assist in choosing vital candidate genes for interruption, a comparison of genes active during critical insect development stages—specifically, the larval and pupal stadia—was performed. The larva serve a vital role in the colony by performing the majority of digestion of complex foods, and this stadium constitutes the insect's most active life stage. The pupa stage immediately follows the larva, and because this stadium is critical to development but does not feed, it was used for comparison. Modern sequencing technology was used to identify genes and compare the two stages. From the thousands of sequenced genes investigated, various gene interruption targets were identified for disrupting vital life processes.

Technical Abstract:

Solenopsis invicta is an invasive species that has been introduced to multiple continents. One such area, the southern United States, has a tragic history of multiple unsuccessful control projects using powerful pesticides over vast ranges, resulting in substantial non-target effects across trophic levels. With the advent of next generation sequencing and RNAi technology, new control methods are available. A robust genome-guided transcriptome assembly was used to investigate gene expression differences between *S. invicta* larvae and pupae. These life stages differ in many physiological processes; of special importance is the vital role of *S. invicta* larvae as the colonies' "communal gut." Differentially expressed transcripts were identified related to many important physiological processes, including digestion, development, cell regulation and hormone signaling. This dataset provides essential developmental knowledge that reveals the dramatic changes in gene expression associated with social insect life stage roles, and can be leveraged using RNAi to develop effective control methods.

Title		Approving Official	Date	Prominent Issues	DUR/DURC	App/Disapp
Research Leader:		MICHAEL J GRODOWITZ	12/06/18	N		Approved
LD/ID/CD Dir:						
Area Director:						
ONP NPL1:						
ONP NPL2:						
ONP NPL3:						
ONP DA:						
OTT Director:						